

**Table S7a. Expression QTL (eQTL) analysis for novel CAD loci.**

Region (lead SNP)	Gene	Gene expressed?	Lead SNP monocyte association P- value	Strength <sup>†</sup>
LIPA (rs2246942)	LIPK	NO		
	LIPN	N/A		
	LIPM	N/A		
	ANKRD22		0.6426	2
	STAMBPL1		0.1400	2
	ACTA2		0.0043	2
	FAS		0.0089	2
	CH25H	NO		
	LIPA		1.01E-124	3
	IFIT2		0.7876	3
	IFIT3		0.9306	2
	IFIT1L	NO		
	IFIT1		0.6344	2
	IFIT5		0.3111	2
	SLC16A12		0.9830	3
	PANK1		0.9559	1
IL5 (rs2706399)	IL3	NO		
	CSF2	NO		
	PDLIM4	NO		
	P4HA2		0.9575	1
	SLC22A4		0.0518	2
	SLC22A5		0.7884	2
	LOC441108	NO		
	IRF1		0.1019	3
	IL5	NO		
	RAD50		6.65E-06	2
	IL13	NO		
	IL4	NO		
	KIF3A	NO		
	CCNI2	N/A		
	SEPT8	N/A		
	ANKRD43	NO		
	SHROOM1		0.0194	1
	GDF9	NO		
	UQCRCQ		0.2126	3
	LEAP2		0.1657	2
	AFF4		0.8323	2
TRIB1 (rs17321515)	ZCCHC10	NO		
	ZNF572	NO		
	SQLE		0.9429	2
	KIAA0196		0.6054	3
	NSMCE2		0.9458	2
ABCG8 (rs4299376)	TRIB1		0.9259	3
	THADA		0.5084	2
	LOC728819	N/A		
	PLEKHH2	NO		
	DYNC2LI1		0.3672	2
	ABCG5	NO		
	ABCG8	NO		
	LRPPRC		0.8337	2
	PPM1B		0.8186	1
	SLC3A1	NO		
	PREPL		0.5951	2

<sup>†</sup>Key (Proportion of all Probes)

1 = Weak (0-20%)

2 = Medium (20-80%)

3 = Strong (80-100%)

Table S7b. Conditional analysis of expression QTL (eQTL) loci.

Gene	Lead SNP	Lead SNP monocyte association P- value	Strength <sup>†</sup>	Secondary SNP used for conditional analysis (r <sup>2</sup> with lead SNP)	Secondary SNP monocyte association P-value	P-value of lead SNP when conditioned on secondary SNP	Independent eQTL signal?	Proxy for secondary SNP in CAD meta-analysis (r <sup>2</sup> )	P value for CAD association with proxy SNP
<i>LIPA</i>	rs2246942	1.01E-124	3	rs2250781 (0.492)	1.54E-96	1.63E-46	Yes	rs2250781 (1)	2.31E-05
<i>RAD50</i>	rs2706399	6.65E-06	2	rs17772583 (0.181)	2.58E-23	0.6698	No	rs2069812 (0.759)	0.20

Conditional analysis of the lead *LIPA* SNP on a secondary SNP at the same locus that is also associated with gene expression shows that the lead SNP at the *LIPA* locus has a strong independent effect on *LIPA* expression levels.  
Conditional analysis of the lead *IL5* SNP on a second nearby SNP that is also associated with *RAD50* gene expression shows that the observed eQTL association with the *IL5* SNP is probably due to LD with the *RAD50* SNP.